

# Studies of Genetic Variability in Yield and Yield Contributing Traits of Foxtail Millet

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#### ABSTRACT

Foxtail millet (*Setaria italica* L.) is an important crop of the semi-arid tropics in India. The present study was conducted to evaluate the foxtail millet genotypes to assess the magnitude of variability and to understand the heritable component of variation present in the biometrical characters. Significant variation was recorded among the genotypes for various yield and yield contributing traits studied. High values for phenotypic co-efficient (PCV) and genotypic co-efficient (GCV) was recorded for grain weight followed by panicle weight and straw yield. High heritability and high genetic advance was recorded for panicle weight, panicle length, number of productive tillers per plants, grain weight and straw yield indicating that these characters were controlled by additive gene effects. Selection based on these characters would be effective for future foxtail millet crop improvement program. Moderate heritability coupled with moderate genetic advance (as percent of mean) was observed for chlorophyll content (SPAD). Threshing percentage showed low heritability as well as low genetic advance.

Key words : Foxtail millet, Genetic advance, Heritability, Variability.

Foxtail millet is a  $C_4$  plant, widely distributed in warm and temperate parts of the world. It is one of the important small millets cultivated in 26 countries with annual production of 2.9 million metric tons from the area of 3.5 m ha. Foxtail millet ranks second in the world's total production of millets and is an important staple food for millions of people in Southern Europe and Asia (Marathee, 1993). Regardless of breeding objective, a critical step is identifying sufficient genetic variation to meet that objective, simply, genetic variation must exist to achieve genetic improvement (Poehlman, 1987). Hence genetic variability of any crop species becomes fundamental to its survival and for its improvement through plant breeding. Genetic variability in any crop can be characterized by adequate evaluation and genetic characterization of the existing germplasm collections. Successful development of new cultivars depends largely on the availability of source germplasm with desirable genetic variability for traits such as improved grain quality and fodder yield. Estimation of genetic variability and genetic advance gives an idea of the possible improvement of the characters through selection.

## MATERIALS AND METHODS

Ten yield contributing characteristics were taken to assess the magnitude of heritable variability among 15 genotypes of foxtail millet. The study was conducted at Regional Agricultural Research Station, Nandyal, Andhra Pradesh during Kharif 2011 under rainfed conditions. The experiment was laid out in a randomized block design (RBD) with three replications. Five plants were randomly selected for recording data on 10 characters viz: days to 50% flowering, plant height, number of productive tillers per plant, panicle length, chlorophyll content (SPAD), panicle weight, grain weight, straw yield, days to maturity and threshing per centage. The data were subjected to statistical analysis. Phenotypic and genotypic variances were estimated according to the formula given by Lush (1940), PCV and GCV were computed based on the methods given by Burton (1952). The heritability was computed based on the methods given by Falconer (1986) and genetic advance was estimated according to the formula given by Johnson et al., (1955). The mean data of five plants over three replications were used for statistical analysis.

### **RESULTS AND DISCUSSION**

The analysis of variance revealed significant differences among the genotypes for all the characters studied indicating that the data generated from the above material would yield reliable information. The estimates of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h<sup>2</sup>) and genetic advance as percent of mean (GAM) are presented in Table. 1.

A wide range of variation was recorded for plant height, number of productive tillers per plant, panicle length, chlorophyll content (SPAD), panicle weight, grain weight and threshing per centage. The estimates of PCV ranged from 3.6 for days to maturity to 25.0 for grain weight and the corresponding values for GCV were 3.5 for days to maturity to 22.1 for straw yield respectively. Grain weight showed the highest PCV and GCV of variation. Panicle length and number of productive tillers per plant showed moderate estimates for PCV and GCV. In general the differences between PCV and GCV were less for all the traits indicating the ample scope for improvement through selection. Low values of PCV and GCV were observed for days to 50% flowering, days to maturity and plant height indicating narrow range of variability for these traits there by restricting the scope for selection.

Heritability gives the information on the magnitude of variation that is due to genetic differences among quantitative traits. Since heritability is also influenced by environment, the information on heritability alone may not help in pinpointing characters enforcing selection. Heritability estimates in conjunction with the predicted genetic advance will be more reliable (Johnson et al., 1955). The heritability values for different yield traits ranged from 0.9% to 96.9%. Days to maturity, panicle weight, panicle length and straw yield show high heritability. Chlorophyll content showed moderate heritability. The heritability estimates were low for threshing per centage. High heritability indicates the amenability of the traits in the selection process. In the present investigation, grain weight, panicle weight, panicle length, number of productive tillers per plant and straw yield showed high heritability and high genetic

advance which are due to additive gene effect and selection would be rewarding. Similar results were also reported by Appadurai et al., (1977) in ragi and Natarajan et al. (1978) in proso millet. Moderate heritability coupled with moderate genetic advance was observed for chlorophyll content indicating the operation of both additive and non additive gene action in the inheritance of the trait. Threshing percentage showed low heritability as well as genetic advance besides narrow range of variability restricting the scope for improvement through selection. Low heritability coupled with low genetic advance for the trait indicated that this trait is controlled by environmental effects and simple selection would be ineffective. According to Panse (1957), if there is nonadditive gene effect, the expected genetic advance would be low and if there is additive gene effect, a high genetic advance may be expected. Taking into consideration the amount of variability, heritability and genetic advance as per cent of mean in the present study it may be concluded that simple phenotypic selection would be effective for panicle weight, panicle length, number of productive tillers per plant and grain weight and would respond favorably for selection for developing high yielding varieties.

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Characters	Mean	Range	PCV	GCV	Heritability	Genetic Advance	Genetic Advance as % of mean
Days to 50% Flowering	43.8	41.0- 46.0	5.3	4.5	72.0	3.5	7.8
Plant Height (cm)	116.9	94.7-127.1	10.3	8.8	73.1	18.0	15.4
Number of Productive tillers/Plant	3.0	2.4- 4.3	18.2	15.2	69.6	0.8	26.1
Panicle Length (cm)	19.5	10.0-24.0	19.3	17.4	81.7	6.3	32.4
Chlorophyll content (SPAD)	39.9	33.2-48.4	11.9	9.1	58.2	5.7	14.3
Panicle Weight (g)	2.7	1.6- 3.5	21.8	20.4	87.6	1.1	39.3
Grain Weight (g)	2.2	1.5- 3.0	25.0	20.5	67.4	0.8	34.7
Straw Yield (Kg)	2.5	1.7- 3.5	24.7	22.1	79.6	1.0	40.5
Days to Maturity	81.9	77.3-85.0	3.6	3.5	96.9	5.8	7.1
Threshing %	80.2	71.5-87.1	10.1	1.0	0.9	0.2	0.2

Table 1. Genetic parameters for yield and yield contributing traits in Foxtail Millet.

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